



## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/729,571A  
Source: IFWO  
Date Processed by STIC: 6/24/04

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
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IFWO

## RAW SEQUENCE LISTING

DATE: 06/24/2004

PATENT APPLICATION: US/10/729,571A

TIME: 10:33:04

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06242004\J729571A.raw

3 <110> APPLICANT: Anderson et al.  
 5 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)  
 7 <130> FILE REFERENCE: ASZD-P01-007  
 9 <140> CURRENT APPLICATION NUMBER: 10/729,571A  
 10 <141> CURRENT FILING DATE: 2003-12-05  
 12 <150> PRIOR APPLICATION NUMBER: 60/435,272  
 13 <151> PRIOR FILING DATE: 2002-12-20  
 15 <150> PRIOR APPLICATION NUMBER: 60/435,167  
 16 <151> PRIOR FILING DATE: 2002-12-20  
 18 <150> PRIOR APPLICATION NUMBER: 60/435,087  
 19 <151> PRIOR FILING DATE: 2002-12-20  
 21 <150> PRIOR APPLICATION NUMBER: 60/435,527  
 22 <151> PRIOR FILING DATE: 2002-12-20  
 24 <160> NUMBER OF SEQ ID NOS: 76  
 26 <170> SOFTWARE: PatentIn version 3.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 768  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: H. pylori  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)..(768)  
 36 <400> SEQUENCE: 1

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39	1			5					10					15			
41	aaa	agc	ctt	tta	aaa	gcg	cga	ttg	ttt	gat	gaa	atc	atc	tac	tat	ggc	96
42	Lys	Ser	Leu	Leu	Lys	Ala	Arg	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
43				20					25					30			
45	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
46	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
47				35					40					45			
49	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cat	gag	att	gaa	192
50	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Glu	Ile	Glu	
51		50						55				60					
53	tta	ttg	att	gtg	gca	tgc	aac	acc	gcg	agc	gct	ctg	gct	tta	gaa	gag	240
54	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
55	65				70				75					80			
57	atg	caa	aag	tat	tct	aaa	atc	cct	att	gtg	ggc	gtg	att	gag	cca	agc	288
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59				85					90					95			
61	att	tta	gcg	atc	aag	cgg	caa	gtg	gaa	gat	aaa	aac	gcc	cct	att	tta	336
62	Ile	Leu	Ala	Ile	Lys	Arg	Gln	Val	Glu	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
63				100					105					110			

pp 1,3,5  
 Does Not Comply  
 Corrected Diskette Needed

insert (global error)

<220> wherever <221>, <222>, or <223> is shown.

MANDATORY.

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66 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
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69 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gct act tct ctt      432
70 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
71      130      135      140
73 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
74 Phe Val Pro Leu Ile Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
75 145      150      155      160
77 act tgc atg cat tat tat ttc act ccc tta gag att tta ccc gaa gtg      528
78 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
79      165      170      175
81 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
82 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
83      180      185      190
85 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
86 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
87      195      200      205
89 cat tcg ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
90 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
91      210      215      220
93 aaa aac aat gca tgc aca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
94 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
95 225      230      235      240
97 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
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113      20      25      30
116 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
117      35      40      45
120 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
121      50      55      60
124 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
125 65      70      75      80
128 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
129      85      90      95
132 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
133      100      105      110
136 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
137      115      120      125
140 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu

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145 145      150      155      160
148 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
149      165      170      175
152 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
153      180      185      190
156 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
157      195      200      205
160 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
161      210      215      220
164 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
165 225      230      235      240
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176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(768)
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182 1      5      10      15
184 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
185 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
186      20      25      30
188 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
189 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
190      35      40      45
192 caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa      192
193 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
194      50      55      60
196 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag      240
197 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
198 65      70      75      80
200 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
201 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
202      85      90      95
204 att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta      336
205 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
206      100      105      110
208 gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
209 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
210      115      120      125
212 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
213 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
214      130      135      140

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&lt;220&gt; insert

## RAW SEQUENCE LISTING

DATE: 06/24/2004

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TIME: 10:33:04

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06242004\J729571A.raw

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218 145      150      155      160
220 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
221 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
222      165      170      175
224 att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag      576
225 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
226      180      185      190
228 ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
229 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
230      195      200      205
232 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt      672
233 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
234      210      215      220
236 aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
237 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
238 225      230      235      240
240 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
241 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
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245 <211> LENGTH: 255
246 <212> TYPE: PRT
247 <213> ORGANISM: H. pylori
249 <400> SEQUENCE: 4
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256      20      25      30
259 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
260      35      40      45
263 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
264      50      55      60
267 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
268 65      70      75      80
271 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
272      85      90      95
275 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
276      100      105      110
279 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
280      115      120      125
283 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
284      130      135      140
287 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
288 145      150      155      160
291 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
292      165      170      175
295 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu

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DATE: 06/24/2004

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TIME: 10:33:04

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06242004\J729571A.raw

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296      180      185      190
299 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
300      195      200      205
303 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
304      210      215      220
307 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
308 225      230      235      240
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317 <213> ORGANISM: H. pylori
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328 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
329      20      25      30
331 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
332 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
333      35      40      45
335 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
336 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
337      50      55      60
339 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
340 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
341 65      70      75      80
343 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
344 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
345      85      90      95
347 att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta      336
348 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
349      100      105      110
351 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc      384
352 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
353      115      120      125
355 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
356 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
357      130      135      140
359 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
360 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
361 145      150      155      160
363 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg      528
364 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
365      165      170      175

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*insert***IMPORTANT:**

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

*<220>*

**VERIFICATION SUMMARY**

DATE: 06/24/2004

PATENT APPLICATION: US/10/729,571A

TIME: 10:33:05

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06242004\J729571A.raw